



OIPE

RAW SEQUENCE LISTING

DATE: 04/30/2004

PATENT APPLICATION: US/09/966,724B

TIME: 10:39:42

Input Set : A:\1107_00193.txt

Output Set: N:\CRF4\04302004\I966724B.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BURRELL, MARILEE

7 HILL, DAVID E.

8 KINZLER, KENNETH W.

9 VOGELSTEIN, BERT

11 (ii) TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

12 HUMAN TUMORS

14 (iii) NUMBER OF SEQUENCES: 5

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

18 (B) STREET: 1001 G STREET, N.W.

19 (C) CITY: WASHINGTON

20 (D) STATE: D.C.

21 (E) COUNTRY: USA

22 (F) ZIP: 20001

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/966,724B

C--> 32 (B) FILING DATE: 01-Oct-2001

33 (C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: KAGAN, SARAH A.

37 (B) REGISTRATION NUMBER: 32,141

38 (C) REFERENCE/DOCKET NUMBER: 01107.42798

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 202-508-9100

42 (B) TELEFAX: 202-508-9299

43 (C) TELEX: 197430 BBMB UT

Does Not Comply
Corrected Diskette Needed

(pg. 3-4)

ERRORED SEQUENCES

528 (2) INFORMATION FOR SEQ ID NO: 5:

530 (i) SEQUENCE CHARACTERISTICS:

531 (A) LENGTH: 489 amino acids

532 (B) TYPE: amino acid

533 (D) TOPOLOGY: linear

535 (ii) MOLECULE TYPE: protein

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537      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
539 Met Cys Asn Thr Asn Met Ser Val Ser Thr Glu Gly Ala Ala Ser Thr
540   1           5           10           15
542 Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
543           20           25           30
545 Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Asn Asp Thr Tyr
546           35           40           45
548 Thr Met Lys Glu Ile Ile Phe Tyr Ile Gly Gln Tyr Ile Met Thr Lys
549           50           55           60
551 Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
552   65           70           75           80
554 Leu Leu Gly Asp Val Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
555           85           90           95
557 Arg Lys Ile Tyr Ala Met Ile Tyr Arg Asn Leu Val Ala Val Ser Gln
558           100          105          110
560 Gln Asp Ser Gly Thr Ser Leu Ser Glu Ser Arg Arg Gln Pro Glu Gly
561           115          120          125
563 Gly Ser Asp Leu Lys Asp Pro Leu Gln Ala Pro Pro Glu Glu Lys Pro
564           130          135          140
566 Ser Ser Ser Asp Leu Ile Ser Arg Leu Ser Thr Ser Ser Arg Arg Arg
567  145           150          155          160
569 Ser Ile Ser Glu Thr Glu Glu Asn Thr Asp Glu Leu Pro Gly Glu Arg
570           165          170          175
572 His Arg Lys Arg Arg Arg Ser Leu Ser Phe Asp Pro Ser Leu Gly Leu
573           180          185          190
575 Cys Glu Leu Arg Glu Met Cys Ser Gly Gly Thr Ser Ser Ser Ser Ser
576           195          200          205
578 Ser Ser Ser Glu Ser Thr Glu Thr Pro Ser His Gln Asp Leu Asp Asp
579           210          215          220
581 Gly Val Ser Glu His Ser Gly Asp Cys Leu Asp Gln Asp Ser Val Ser
582  225          230          235          240
584 Asp Gln Phe Ser Val Glu Phe Glu Val Glu Ser Leu Asp Ser Glu Asp
585           245          250          255
587 Tyr Ser Leu Ser Asp Glu Gly His Glu Leu Ser Asp Glu Asp Asp Glu
588           260          265          270
590 Val Tyr Arg Val Thr Val Tyr Gln Thr Gly Glu Ser Asp Thr Asp Ser
591           275          280          285
593 Phe Glu Gly Asp Pro Glu Ile Ser Leu Ala Asp Tyr Trp Lys Cys Thr
594           290          295          300
596 Ser Cys Asn Glu Met Asn Pro Pro Leu Pro Ser His Cys Lys Arg Cys
597  305          310          315          320
599 Trp Thr Leu Arg Glu Asn Trp Leu Pro Asp Asp Lys Gly Lys Asp Lys
600           325          330          335
602 Val Glu Ile Ser Glu Lys Ala Lys Leu Glu Asn Ser Ala Gln Ala Glu
603           340          345          350
605 Glu Gly Leu Asp Val Pro Asp Gly Lys Lys Leu Thr Glu Asn Asp Ala
606           355          360          365
608 Lys Glu Pro Cys Ala Glu Glu Asp Ser Glu Glu Lys Ala Glu Gln Thr
609           370          375          380

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611 Pro Leu Ser Gln Glu Ser Asp Asp Tyr Ser Gln Pro Ser Thr Ser Ser
612 385 390 395 400
614 Ser Ile Val Tyr Ser Ser Gln Glu Ser Val Lys Glu Leu Lys Glu Glu
615 405 410 415
617 Thr Gln His Lys Asp Glu Ser Val Glu Ser Ser Phe Ser Leu Asn Ala
618 420 425 430
620 Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly Cys Ile
621 435 440 445
623 Val His Gly Lys Thr Gly His Leu Met Ser Cys Phe Thr Cys Ala Lys
624 450 455 460
626 Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln Pro Ile
627 465 470 475 480
629 Gln Met Ile Val Leu Ser Tyr Phe Asn
630 485
E--> 633 1

delete

VERIFICATION SUMMARY

DATE: 04/30/2004

PATENT APPLICATION: US/09/966,724B

TIME: 10:39:44

Input Set : A:\1107_00193.txt

Output Set: N:\CRF4\04302004\I966724B.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:633 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5